

METHOD OF OBTAINING PROTEIN DIVERSITY

ABSTRACT OF THE DISCLOSURE

The present invention provides a method that can facilitate structure determination of target proteins by x-ray crystallography. It is a method of rational
5 crystallization of members of a target protein family obtained through specific amplification of corresponding genes from natural diversity. The method makes broad biodiversity accessible through sampling and ecological enrichment of diverse high-temperature ecosystems containing thermophilic microorganisms including uncultivable and previously unknown organisms. The method provides means to
10 circumvent many potential problems and bottlenecks in crystal structure determination by selection of suitable proteins directly from nature. The invention combines methods of accessing and screening vast natural diversity and the inherent suitability of thermostable proteins for crystallization in order to maximize probability of successful structure determination.

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